

PCT09

RAW SEQUENCE LISTING  
 PATENT APPLICATION: US/09/787,923

DATE: 10/26/2001  
 TIME: 14:59:28

Input Set : A:\ES.txt  
 Output Set: N:\CRF3\10262001\I787923.raw

3 <110> APPLICANT: SANSON, ALAIN  
 4 RUSSO-MARIE, FRANCOISE  
 5 NEUMANN, JEAN-MICHEL  
 6 CORDIER-OCHSENBEIN, FRANCOISE  
 7 GUEROIS, RAPHAEL  
 9 <120> TITLE OF INVENTION: CHEMICAL STRUCTURE HAVING AN AFFINITY FOR A PHOSPHOLIPID AND  
 LABELLING  
 10 COMPOUND, DIAGNOSIS KIT, AND DRUG COMPRISING THIS STRUCTURE  
 12 <130> FILE REFERENCE: 205399US-0-XPCT  
 14 <140> CURRENT APPLICATION NUMBER: US 09/787,923  
 15 <141> CURRENT FILING DATE: 2001-04-02  
 17 <150> PRIOR APPLICATION NUMBER: FR 98/12366  
 18 <151> PRIOR FILING DATE: 1998-10-02  
 20 <150> PRIOR APPLICATION NUMBER: PCT/FR99/02329  
 21 <151> PRIOR FILING DATE: 1999-09-30  
 23 <160> NUMBER OF SEQ ID NOS: 5  
 25 <170> SOFTWARE: PatentIn version 3.1  
 27 <210> SEQ ID NO: 1  
 28 <211> LENGTH: 346  
 29 <212> TYPE: PRT  
 30 <213> ORGANISM: Homo sapiens  
 32 <400> SEQUENCE: 1  
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 35 1 5 10 15  
 38 Glu Glu Gln Glu Tyr Val Gln Thr Val Lys Ser Ser Lys Gly Gly Pro  
 39 20 25 30  
 42 Gly Ser Ala Val Ser Pro Tyr Pro Thr Phe Asn Pro Ser Ser Asp Val  
 43 35 40 45  
 46 Ala Ala Leu His Lys Ala Ile Met Val Lys Gly Val Asp Glu Ala Thr  
 47 50 55 60  
 50 Ile Ile Asp Ile Leu Thr Lys Arg Asn Asn Ala Gln Arg Gln Gln Ile  
 51 65 70 75 80  
 54 Lys Ala Ala Tyr Leu Gln Glu Thr Gly Lys Pro Leu Asp Glu Thr Leu  
 55 85 90 95  
 58 Lys Lys Ala Leu Thr Gly His Leu Glu Glu Val Val Leu Ala Leu Leu  
 59 100 105 110  
 62 Lys Thr Pro Ala Gln Phe Asp Ala Asp Glu Leu Arg Ala Ala Met Lys  
 63 115 120 125  
 66 Gly Leu Gly Thr Asp Glu Asp Thr Leu Ile Glu Ile Leu Ala Ser Arg  
 67 130 135 140  
 70 Thr Asn Lys Glu Ile Arg Asp Ile Asn Arg Val Tyr Arg Glu Glu Leu  
 71 145 150 155 160  
 74 Lys Arg Asp Leu Ala Lys Asp Ile Thr Ser Asp Thr Ser Gly Asp Phe  
 75 165 170 175  
 78 Arg Asn Ala Leu Leu Ser Leu Ala Lys Gly Asp Arg Ser Glu Asp Phe  
 79 180 185 190  
 82 Gly Val Asn Glu Asp Leu Ala Asp Ser Asp Ala Arg Ala Leu Tyr Glu  
 83 195 200 205

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86 Ala Gly Glu Arg Arg Lys Gly Thr Asp Val Asn Val Phe Asn Thr Ile  
87 210 215 220  
90 Leu Thr Thr Arg Ser Tyr Pro Gln Leu Arg Arg Val Phe Gln Lys Tyr  
91 225 230 235 240  
94 Thr Lys Tyr Ser Lys His Asp Met Asn Lys Val Leu Asp Leu Glu Leu  
95 245 250 255  
98 Lys Gly Asp Ile Glu Lys Cys Leu Thr Ala Ile Val Lys Cys Ala Thr  
99 260 265 270  
102 Ser Lys Pro Ala Phe Phe Ala Glu Lys Leu His Gln Ala Met Lys Gly  
103 275 280 285  
106 Val Gly Thr Arg His Lys Ala Leu Ile Arg Ile Met Val Ser Arg Ser  
107 290 295 300  
110 Glu Ile Asp Met Asn Asp Ile Lys Ala Phe Tyr Gln Lys Met Tyr Gly  
111 305 310 315 320  
114 Ile Ser Leu Cys Gln Ala Ile Leu Asp Glu Thr Lys Gly Asp Tyr Glu  
115 325 330 335  
118 Lys Ile Leu Val Ala Leu Cys Gly Gly Asn  
119 340 345  
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123 <211> LENGTH: 320  
124 <212> TYPE: PRT  
125 <213> ORGANISM: Homo sapiens  
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130 1 5 10 15  
133 Glu Arg Ala Asp Ala Glu Thr Leu Arg Lys Ala Met Lys Gly Leu Gly  
134 20 25 30  
137 Thr Asp Glu Glu Ser Ile Leu Thr Leu Leu Thr Ser Arg Ser Asn Ala  
138 35 40 45  
141 Gln Arg Gln Glu Ile Ser Ala Ala Phe Lys Thr Leu Phe Gly Arg Asp  
142 50 55 60  
145 Leu Leu Asp Asp Leu Lys Ser Glu Leu Thr Gly Lys Phe Glu Lys Leu  
146 65 70 75 80  
149 Ile Val Ala Leu Met Lys Pro Ser Arg Leu Tyr Asp Ala Tyr Glu Leu  
150 85 90 95  
153 Lys His Ala Leu Lys Gly Ala Gly Thr Asn Glu Lys Val Leu Thr Glu  
154 100 105 110  
157 Ile Ile Ala Ser Arg Thr Pro Glu Glu Leu Arg Ala Ile Lys Gln Val  
158 115 120 125  
161 Tyr Glu Glu Tyr Gly Ser Ser Leu Glu Asp Asp Val Val Gly Asp  
162 130 135 140  
165 Thr Ser Gly Tyr Tyr Gln Arg Met Leu Val Val Leu Leu Gln Ala Asn  
166 145 150 155 160  
169 Arg Asp Pro Asp Ala Gly Ile Asp Glu Ala Gln Val Glu Gln Asp Ala  
170 165 170 175  
173 Gln Ala Leu Phe Gln Ala Gly Glu Leu Lys Trp Gly Thr Asp Glu Glu  
174 180 185 190  
177 Lys Phe Ile Thr Ile Phe Gly Thr Arg Ser Val Ser His Leu Arg Lys  
178 195 200 205

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181 Val Phe Asp Lys Tyr Met Thr Ile Ser Gly Phe Gln Ile Glu Glu Thr  
182 210 215 220  
185 Ile Asp Arg Glu Thr Ser Gly Asn Leu Glu Gln Leu Leu Leu Ala Val  
186 225 230 235 240  
189 Val Lys Ser Ile Arg Ser Ile Pro Ala Tyr Leu Ala Glu Thr Leu Tyr  
190 245 250 255  
193 Tyr Ala Met Lys Gly Ala Gly Thr Asp Asp His Thr Leu Ile Arg Val  
194 260 265 270  
197 Met Val Ser Arg Ser Glu Ile Asp Leu Phe Asn Ile Arg Lys Glu Phe  
198 275 280 285  
201 Arg Lys Asn Phe Ala Thr Ser Leu Tyr Ser Met Ile Lys Gly Asp Thr  
202 290 295 300  
205 Ser Gly Asp Tyr Lys Lys Ala Leu Leu Leu Cys Gly Glu Asp Asp  
206 305 310 315 320  
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210 <211> LENGTH: 323  
211 <212> TYPE: PRT  
212 <213> ORGANISM: Homo sapiens  
214 <400> SEQUENCE: 3  
216 Met Ala Ser Ile Trp Val Gly His Arg Gly Thr Val Arg Asp Tyr Pro  
217 1 5 10 15  
220 Asp Phe Ser Pro Ser Val Asp Ala Glu Ala Ile Gln Lys Ala Ile Arg  
221 20 25 30  
224 Gly Ile Gly Thr Asp Glu Lys Met Leu Ile Ser Ile Leu Thr Glu Arg  
225 35 40 45  
228 Ser Asn Ala Gln Arg Gln Leu Ile Val Lys Glu Tyr Gln Ala Ala Tyr  
229 50 55 60  
232 Gly Lys Glu Leu Lys Asp Asp Leu Lys Gly Asp Leu Ser Gly His Phe  
233 65 70 75 80  
236 Glu His Leu Met Val Ala Leu Val Thr Pro Pro Ala Val Phe Asp Ala  
237 85 90 95  
240 Lys Gln Leu Lys Lys Ser Met Lys Gly Ala Gly Thr Asn Glu Asp Ala  
241 100 105 110  
244 Leu Ile Glu Ile Leu Thr Thr Arg Thr Ser Arg Gln Met Lys Asp Ile  
245 115 120 125  
248 Ser Gln Ala Tyr Tyr Thr Val Tyr Lys Lys Ser Leu Gly Asp Asp Ile  
249 130 135 140  
252 Ser Ser Glu Thr Ser Gly Asp Phe Arg Lys Ala Leu Leu Thr Leu Ala  
253 145 150 155 160  
256 Asp Gly Arg Arg Asp Glu Ser Leu Lys Val Asp Glu His Leu Ala Lys  
257 165 170 175  
260 Gln Asp Ala Gln Ile Leu Tyr Lys Ala Gly Glu Asn Arg Trp Gly Thr  
261 180 185 190  
264 Asp Glu Asp Lys Phe Thr Glu Ile Leu Cys Leu Arg Ser Phe Pro Gln  
265 195 200 205  
268 Leu Lys Leu Thr Phe Asp Glu Tyr Arg Asn Ile Ser Gln Lys Asp Ile  
269 210 215 220  
272 Val Asp Ser Ile Lys Gly Glu Leu Ser Gly His Phe Glu Asp Leu Leu  
273 225 230 235 240

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276 Leu Ala Ile Val Asn Cys Val Arg Asn Thr Pro Ala Phe Leu Ala Glu  
277 245 250 255  
280 Arg Leu His Arg Ala Leu Lys Gly Ile Gly Thr Asp Glu Phe Thr Leu  
281 260 265 270  
284 Asn Arg Ile Met Val Ser Arg Ser Glu Ile Asp Leu Leu Asp Ile Arg  
285 275 280 285  
288 Thr Glu Phe Lys Lys His Tyr Gly Tyr Ser Leu Tyr Ser Ala Ile Lys  
289 290 295 300  
292 Ser Asp Thr Ser Gly Asp Tyr Glu Ile Thr Leu Leu Lys Ile Cys Gly  
293 305 310 315 320  
296 Gly Asp Asp  
300 <210> SEQ ID NO: 4  
301 <211> LENGTH: 85  
302 <212> TYPE: PRT  
303 <213> ORGANISM: Homo sapiens  
305 <400> SEQUENCE: 4  
307 Met Ala Thr Lys Gly Gly Thr Val Lys Ala Ala Ser Gly Phe Asn Ala  
308 1 5 10 15  
311 Met Glu Asp Ala Gln Thr Leu Arg Lys Ala Met Lys Gly Leu Gly Thr  
312 20 25 30  
315 Asp Glu Asp Ala Ile Ile Ser Val Leu Ala Tyr Arg Asn Thr Ala Gln  
316 35 40 45  
319 Arg Gln Glu Ile Arg Thr Ala Tyr Lys Ser Thr Ile Gly Arg Asp Leu  
320 50 55 60  
323 Ile Asp Asp Leu Lys Ser Glu Leu Ser Gly Asn Phe Glu Gln Val Ile  
324 65 70 75 80  
327 Val Gly Met Met Thr  
328 85  
331 <210> SEQ ID NO: 5  
332 <211> LENGTH: 235  
333 <212> TYPE: PRT  
334 <213> ORGANISM: Homo sapiens  
336 <400> SEQUENCE: 5  
338 Pro Thr Val Leu Tyr Asp Val Gln Glu Leu Gln Arg Lys Ala Met Lys  
339 1 5 10 15  
342 Gly Ala Gly Thr Asp Glu Gly Cys Leu Ile Glu Ile Leu Ala Ser Arg  
343 20 25 30  
346 Thr Pro Glu Glu Ile Arg Arg Ile Asn Gln Thr Tyr Gln Leu Gln Tyr  
347 35 40 45  
350 Gly Arg Ser Leu Glu Asp Asp Ile Arg Ser Asp Thr Ser Phe Met Phe  
351 50 55 60  
354 Gln Arg Val Leu Val Ser Leu Ser Ala Gly Gly Arg Asp Glu Gly Asn  
355 65 70 75 80  
358 Tyr Leu Asp Asp Ala Leu Val Arg Gln Asp Ala Gln Asp Leu Tyr Glu  
359 85 90 95  
362 Ala Gly Glu Lys Lys Trp Gly Thr Asp Glu Val Lys Phe Leu Thr Val  
363 100 105 110  
366 Leu Cys Ser Arg Asn Arg Asn His Leu Leu His Val Phe Asp Glu Tyr  
367 115 120 125

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370 Lys Arg Ile Ser Gln Lys Asp Ile Glu Gln Ser Ile Lys Ser Glu Thr  
371 130 135 140  
374 Ser Gly Ser Phe Glu Asp Ala Leu Leu Ala Ile Val Lys Cys Met Arg  
375 145 150 155 160  
378 Asn Lys Ser Ala Tyr Phe Ala Glu Lys Leu Tyr Lys Ser Met Lys Gly  
379 165 170 175  
382 Leu Gly Thr Asp Asp Asn Thr Leu Ile Arg Val Met Val Ser Arg Ala  
383 180 185 190  
386 Glu Ile Asp Met Leu Asp Ile Arg Ala His Phe Lys Arg Leu Tyr Gly  
387 195 200 205  
390 Lys Ser Leu Tyr Ser Phe Ile Lys Gly Asp Thr Ser Gly Asp Tyr Arg  
391 210 215 220  
394 Lys Val Leu Leu Val Leu Cys Gly Gly Asp Asp  
395 225 230 235

**VERIFICATION SUMMARY**

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